

Figure 1
PSSP

1 GGCACGAGCCAGCTCCTTCCTGTTCCCTGGCGGGCCCTCGCTTCTTCCTCTGGATGGG 60
61 GGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAGGGTGCCCGGCACAACCAGACG 120
121 CCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGGCCATGCTGCTGCTGCTCAC 180
1 M H R P E A M L L L L T 12
181 GCTTGCCCTCCTGGGGGGCCCACTGGGCAGGGAAGATGTATGGCCCTGGAGGAGGCAA 240
13 L A L L G G P T W A G K M Y G P G G G K 32
241 GTATTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCTGCGGGTGTCTGTAGG 300
33 Y F S T T E D Y D H E I T G L R V S V G 52
301 TCTTCGCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTGAAACTGGG 360
53 L L L V K S V Q V K L G D S W D V K L G 72
361 AGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACAAAAGT 420
73 A L G G N T Q E V T L Q P G E Y I T K V 92
421 CTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTGTGGTCATGTACACCAGCAAGGACCGCTA 480
93 F V A F Q A F L R G V V M Y T S K D R Y 112
481 TTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCA 540
113 F Y F G K L D G Q I S S A Y P S Q E G Q 132
541 GGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGA 600
133 V L V G I Y G Q Y Q L L G I K S I G P E 152
601 ATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGC 660
153 W N Y P L E E P T T E P P V N L T Y S A 172
661 AAACCTACCCGTGGGTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGGG 720
173 N S P V G R * 179
721 TGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAAT 780
781 AAATAAGCTTCTGCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 825

Figure 2

	10	20	30	40					
1	MHRPEAM	L L L L T L A L L G G P T - W A G K M Y - G P G G G K Y F S T T E	PSSP.AA						
1	M - - - - -	L P L L I L A F L G T P A V L T Q S R Y H G S E T G K H F C I V A	U00964.aa						
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	50	60	70	80					
39	DYDHEI	TGIRVS	VGLLLVK	SVQVKL	GDSW	DVKLGAL	GGNT	PSSP.AA	
35	PEGEPF	VTGTWAS	IKNNII	SISIRL	KFGNNW	SQEYGSS	GRAE	U00964.aa	
<hr/>									
	90	100	110	120					
79	QEVTLQ	PGEYIT	TKVFVA	FQAFLR	GVVMYT	SKDRYFY	FYFGKL	PSSP.AA	
75	I EV KL N P D E T V L G E S G S F Y I F M H O I I I T T S Q P R E L I I G P L	U00964.aa							
<hr/>									
	130	140	150	160					
119	DGQ-ISSA	YP SQEG	QVLVG	GIYG	QQQL	LGIKS	IGFEWN	NYPL	PSSP.AA
115	TGRYVVYS	YPENPNH	VFRGIC	GYYVTG	GLKGM	RYLWG	- - -	U00964.aa	
<hr/>									
	170	180							
158	E E P T T E P P	V N L T Y S A N S P V G R .	PSSP.AA						
152	- - - - -	N V N G T C T - - - - - E	U00964.aa						

Figure 3

